

Remarks

Applicants have been requested to correct drawings Figs. 1 – 8. As described below, the specification has been amended to comply with the correction. No new matter has been added by this Amendment.

The Official Draftsperson has indicated that views are not labeled properly in Figs. 2-5, 7 and 8. The drawings have been corrected and the specification has been amended to correspond with number changes and matters of form as it pertains to 2A-2B, 3A-3B, 4A-4B, 5A-5B, 7A-7B and 8A-8B.

In addition, lines in Fig. 6 have been changed to make them more uniformly thick and well defined.

Numbers and reference characters in all of the drawings have been made more plain and legible.

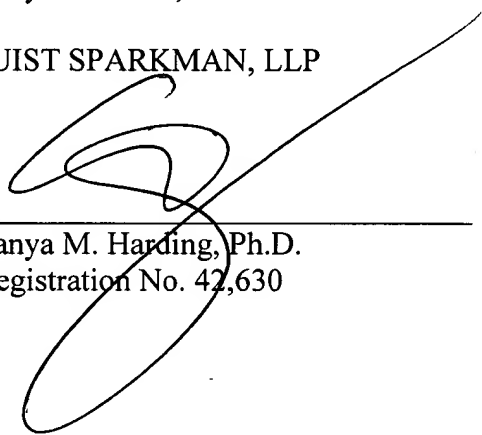
Conclusions

It is believed that this Amendment fully addresses the requested corrections in the Notice Regarding Drawings. Applicants therefore respectfully request that a patent issue in this case. The Official Draftsperson is requested to telephone the undersigned at the number listed below if it may expedite the issuance of the patent.

Respectfully submitted,

KLARQUIST SPARKMAN, LLP

By



Tanya M. Harding, Ph.D.
Registration No. 42,630

One World Trade Center, Suite 1600
121 S.W. Salmon Street
Portland, Oregon 97204
Telephone: (503) 226-7391
Facsimile: (503) 228-9446

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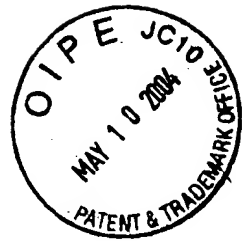
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-950 ACTCA TAAAAACTAG TAGATTGGTT GGTGGTTTC CATGTACCAG
Atp^{proFW} →

-900 AAGGCTTACC CTATTAGTTG AAAGTTGAAA CTTTGTTCCC TACTCAATTC

-850 CTAGTTGTGT AAATGTATGT ATATGTAATG CGTATAAAAC GTAGTACTTA

-800 AATGACTAGG AGTGGTTCTT GAGACCGATG AGAGATGGGA GCAGAACTAA

-750 AGATGATGAC ATAATTAAGA ACGAATTGTA AAGGCTCTTA GGTTTGAATC

-700 CTATTGCGA ATGTTTTTGT CAAAGATAGT GGCGATTTTG AACCAAAGAA

-650 AACATTTAAA AAATCAGTAT CCGGTTACGT TCATGCAAAT AGAAAGTGGT

-600 CTAGGATCTG ATTGTAATTT TAGACTTAAA GAGTCTCTTA AGATTCAATC

-550 CTGGCTGTGT ACAAACTAC AAATAATATA TTTTAGACTA TTTGGCCTTA

-500 ACTAACTTC CACTCATTAT TTACTGAGGT TAGAGAATAG ACTTGCGAAT

-450 AAACACATTC CCGAGAAATA CTCATGATCC CATAATTAGT CAGAGGGTAT

-400 GCCAATCAGA TCTAAGAACA CACATTCCCT CAAATTTTAA TGCACATGTA

-350 ATCATAGTTT AGCACAAATC AAAAATAATG TAGTATTAAA GACAGAAATT

-300 TGTAGACTTT TTTTTGGCGT TAAAGGAAGA CTAAGTTTAT ACGTACATTT

-250 TATTTTAAGT GGAAAACCGA AATTTTCCAT CGAAATATAT GAATTTAGTA

-200 TATATATTTT TGCAATGTAC TATTTTGCTA TTTTGGCAAC TTTCAGTGGA

-150 CTACTACTTT ATTACAATGT GTATGGATGC ATGAGTTTGA GTATACACAT

-100 GTCTAAATGC ATGCTTTGCA AAACGTAACG GACCACAAAA GAGGATCCAT

-50 GCAAATACAT CTCATAGCTT CCTCCATTAT TTTCCGACAC AAACAGAGCA
← Atp^{proRV}

1 ATGACGTCCG TTAACGTAA GTCCTT

FIG. 1

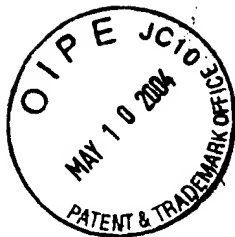
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***Brassica napus* FAE1 promoter:**
(Length: 1588 bp)

FIG. 2A

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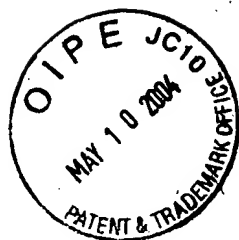


(Continued)

-450 GTTACATAGA TTTGGAAACA CTTCATCTAG CTCATATGG TATGAGTTGG
-400 CATACATAGA AGCAAAAGGA AGGATGAAGA AAGGTAATAA AGTTTGGCAG
-350 ATTGCTTTAG GGTGAGGCTT TAAGTGTAAC AGTGCAGTTT GGGTGGCTCT
-300 AAACAATGTC AAAGCTTCGA CAAATAGTCC TTGGGAACAC TGCATCGACA
-250 GATACCCGGT CAAAATTGAT TCTGATTCAG GTAAGTCAGA GACTCGTGTC
-200 CAAAACGGTC GGTCTTAATA AACGATGTTT GCTCTCTTTC GTTTCTTTTT
-150 ATTTGTTATA ATAATTTGAT GGCTACGATG TTTCTCTTGT TTGTTATGAA
-100 TAAAGAATGC AATGGTGTTT TAGTATTTGA TTGTTTTACA TGTATGTATC
-50 TCTTATTTAC ATGAAATTTT TAAACGCCTA AAAAAAAAAA CGGAATTCGG
1 ATGACGTCCA TTAACGTAAA GCTCCTTTAC CATTACGTCA TAACCAACCT
51 TTTCAACCTT TGCTTCTTTC CGTTAACGGC GATCGTCGCC GGAAAAGCCT
101 ATCGGCTTAC CATAGACGAT CTTCAACCACT TATACTATTC CTATCTCCAA
151 CACAACCTCA TAACCATCGC TCCACTCTTT GCCTTCACCG
← Bnwalk1
← Bnwalk2
← BnproRV

FIG. 2B

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Figure 3. *Lunaria annua* FAE1 promoter:
(Length: 1069 bp)

```
-1100          CG CCGGGGAGTT TCAGCTTAAC CCGTAAAATT
                                     LaproFW →
-1050 GGCCTGTACA TATATTTACC ACTGAGTAAA GACATCAGTT AATGATTTGT
-1000 TGTTACTCAA TTGGGCTAAG TGTATTATTA TATGTGTTGT ATATAATAAA
-950  GGTAGAACGT AAATTTACTA AGAATGTGTT TTTCCAATGT GATTGCTCTT
-900  TGGCCTCTTA GGTTTGAATC CTACTCGAGA AGACTAATTT TAATTTACTG
-850  GCAAAAATAG AAATCAATTT ATAAGTGTTT AAACAAATCG ATGGTATAAC
-800  TGATTAGTGA TCACTCTTAG GTTTTGATCC AACTCGAGTA TTGAGTATTG
-750  AACGCTTTTT TTAAATAAAA TCTTGATTTT TAAATTGGTT TTTTGAGTAA
-700  AAAAGTTCTT AATATTTTCT CTTTGTTTTA ATGGGTTTGT TTTGCATTTT
-650  ATAAGCTTAA TTTTCTAAT TTAATATTTT ATCTATCATC GTCCGTAAAG
-600  TTTTATTTGG CACAACTTG TTTTACTTTT CTACCTTATA ATTTGGGAAC
-550  TGGTTGAGTC AAAGCGTACC GGACAAATAT GTTTTATATT CTTATTTAAG
-500  AATTAACACT CATCTCATAA TTAGTCAGAG GCTAGGGAGA TTCAGCCAAT
-450  CAATGCTAAC AACAAATTC TCTTAATGAT CTAACGATGC TATTTAATAT
-400  TCGGATCAGT ATTCTTAAAT AAGAATATAA AACTAATTCA ATAGTTACAG
-350  ATAAAACTT ATATAGACTT TTTTATTTGG AATATAAAAG TATCAATATA
-300  TTATAGACAA TATTTATAAC GTTAAAAATA CAATATTTAT ATTTTTTATA
-250  TATTTATTTT AAATTGAAAA GCATTACTTC TATCGAAATG AATTTTAGTA
-200  TATTAATTAA TATTTTTTTA ATCGGACTAC TTTCTATTT TGGCACCTTT
-150  CATCTGACTA CTAATTTATT TCAATGTGTA TGCATGCATG AGCATGAGTA
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F16.3A

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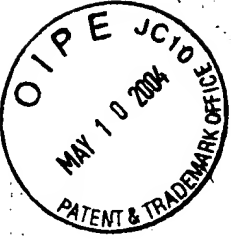
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~~Figure 3 Continued.~~ *Lunaria annua FAE1* promoter:
(Continued)

-100 ATACACATGT CTATATAAAT GCATGTAAAA CGTAACGGAC CACAAAAGTG
-50 GATCCATACA AATACATCTC ATCGCACCCCT CTCCGACACA AAACCTGAACA
1 ATGACGTCTG TGAACGTAAA ACTCCTTTAC CATTACGTCA TAACCAACTT
51 TTTCAACCTC TGTTTCTTCC CACTGACGGG GATCCTCGCC GGAAAAGGCT
101 CTCGTCTTAC CACAAACGAT CTCCACCA
← Lawalk1
← Lawalk2
← LaproRV

FIG. 3B



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[illegible]

FIG. 4A

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~~Figure 4 Continued~~ Alignment of A.t., L.a. and B.n. FAE1 promoters (continued)

A.t. TTGGTTTCCA--TGTACCAGAAGGCTTACCCTAT-TAGTTGAAAGTTGAACTTTGTTC
 L.a. TTGTTACTCAATTGGGCTAAGTGATTATTATAT-GTGTGTATATAATAAGGTAGAAC
 B.n. ACTTGTGCATGTCCATAAAAATACGTATGCTCTTGTGGTGAGCACAGAGAACATCACTT
 * * * * *
 Con. 4 WYKKKWYBCANNTSBRYHARRWKDMKTAYBMTMTNKWGKTGWRHRYWRWRAMBDTVDHHY

A.t. CTAATCAATTCCTAGTTGTGTAAATGT---ATGTATATGTAAT---GCGTATAAAACGTA
 L.a. GTAA--ATTTACTAAGAATGTGTTTTTCCAATGTGATTGCTCTTTGGCCTCTTAGGTTTG
 B.n. ATAA-CATTTACGCTGGTGATAATAGGTCCATGATGGTTTCAAATTGCTTGTTCGGTGT
 * * * * *
 Con. 4 VTAMNNAWTTMCMMDKDDKRTRWWKNNNATGWDDTKYHMWNNGCBTVTMVRYKTD

A.t. GTACTTAAATGACTAGGAGTGGTCTTGAGACCGATGAGAGATGGGAG-CAGAACTAAAG
 L.a. AATCCTACTCGAGAAG-ACTAATTTTAATTTACTGGCAAAAATAGAAA-TCAATTTATAA
 B.n. GGTGGGGC-CGCTATTTTGCTCTCCAACAAGCCTGGAGATCGTAGCGGTCCAAGTACGA
 * * * * *
 Con. 4 RDWSBKRMNYGMBWWKNWSYDVITYWWVDDMCKRKVRRWVRTRGRMRNYMVAWBTahr

A.t. AT--GATGACATAATTA-----AGAACGAATTTGA-AAGG-CTCTTAGGTTTGAATCCT
 L.a. GT--GTTTAAACAAATCGATGGTATAACTGATTAGT-GATCACTCTTAGGTTTGTATCCA
 B.n. GCTAGTTCAACGCTTCGAACGCATACCGGAGCTGACGACAAGTCTTTTCGTTGCGTGCA
 * * * * *
 Con. 4 RYNNGWTBAMAYRRWTMNNNNNNNAKAMCKRAKYWGWNRBVNSTCTTWKSKTTKVRTSCW

A.t. ATTCGAGAATGTTTTTGTCAAAGATAGTGGCGATTTTGAACCAAAGAAAACATTTAAA-A
 L.a. ACTCGAGTATTGAGTATTGAACGCTT-----TTTTTAAATAAAATCTTGATTTTAA-A
 B.n. A--CAAGGA-GACGATGAGAACGGCAA----AATCGGAGTGAGTTGTCCAAGGACATA
 * * * * *
 Con. 4 ANNCRAGDANKDHKWWKWSAAMGVYWNNNNNNNNTYKKARHBARWDVWWSAWKKWHANA

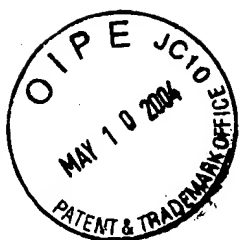
A.t. AATCAGTATCCGGTTAC---GTTTCATGCAAATAGAAAGTGGTCTA---GGATCTGATT-
 L.a. ATTGGTTTTTTGAGTAAAAAAGTTCTTAATATTTTCTCTTTGTTTAAATGGGTTTGT
 B.n. ACCGATGTTGCTGTCGAACGGTTAAGAAAAACATAGCAACGTT----GGGTCGGTTGA
 * * * * *
 Con. 4 AHYSRKKWTBYKRKTMTNNNGTTMWKRMWAWYWKMDMDWBGTYNNNNNGGRTYYGWTKN

A.t. GTAATTTTAGA--CTTAAAGAGTCTC--TTAAGATTCAATCCTGGCT-GTGTACAAAAC
 L.a. TGCATTTTATAAGCTTAATTTTTCTAATTTAATATTTTATCTATCATCGTCCGTAAAGTT
 B.n. TTCTTCGGTTAAGCGAGAACTTCTT--TTTTTCGTTA--CCTTCATGGGCAAGAACTT
 * * * * *
 Con. 4 KKMWTYYKWKANNCKWRAWDHKTCTHNNTTWWMKTYWNNCYWKSMTNGKSHRBAAAVYT

A.t. ACAATAATATA----TTTTAGACTATTTGGCCTTAATAAACTTCCA-CTCATTATTTA
 L.a. TTATTTGGCACAACTTGTTTTACTTTTCTACCTTA--TAATTTGGGAAGTGGTTGAGT-
 B.n. TTCAAAGATAAAATCAAACATTACTACGTCCTCGGATTTCAAACCTTGCTATTGACCATTT
 * * * * *
 Con. 4 WYMWWRRYAHANNNNWDYWWKACTWYKYBVCSSKWWNNYAAYTKSSWNYTSRYRWKTN

A.t. -CTGAGGTTAGAGAA--TAGACTTGCGAATAAACACATTCCTCGAGAAATACTCATGATCC
 L.a. -CAAAGCGTACCGGA--CAAATATGTTT-TATATTCTTATTTAAGAATTAACACTCATCT
 B.n. TGTATACATGCCGAGGCAGAGCCGTGATTGATGTGCTAGAGAAGAACCTAGCCCTAGCA
 * * * * *
 Con. 4 NSWRWRS DTRSMGRANNYARABHYGYKWNTRWBWSHTWBHBRAGAAYWMBMMYBAKCH

Fig. 4B



~~Figure 4 Continued: Alignment of A.t., L.a. and B.n. FAE1 promoters~~

(continued)

CE3

A.t. CATAATTAGTCAGAGGGTATG-----CCAATCAGATCTAAGAACACACATTCCCTC
L.a. CATAATTAGTCAGAGGCTAGGGAGATTGAGCCAATCAATGCTAACAACAAA-ATTCTCTT
B.n. CCGATCGATGTAGAGGC-----ATCAAGATCAACGTTACATAGATTGCG
* * * * *
Con. 4 CMKAWYKAKKYAGAGGSNNNNNNNNNNNNNNNNNNATCARDYYAASRWYAMANAKWYYYKB

A.t. AA--ATTTA--ATGCAC-ATGTAATCAT-----AGTTT-----AGCACAATTCAAAA
L.a. AATGATCTAACGATGCT--ATTTAATATTCCGATCAGTATTCTTAAATAAGAATATAAAA
B.n. AAACACTTCATCTAGCTCAATATGGTATG-----AGTTGGCATACT-AGAAG-CAAAA
* * * * *
Con. 4 AANNAYYTHANNWGCWNNATDTRRTMWKNNNNNNNAGTWKNNNNNNNAKNASAAKNYAAAA

A.t. ATAATGTAGTA-TTAAAGACAGAAATTTGTA--GACTTTTTT---TTGGCGT-TAAAGG
L.a. CTAATTCATAGTTACAGATAAAAACTTATATAGACTTTTTTAT--TTGGAATATAAAAG
B.n. GGAAGGATGAA-GAAAGGTAATAAAGTTTGGCAGATTGCTTTAGGGTCAGGCTTTAAGTG
* * * * *
Con. 4 VKAAKHWKRWANKWAMRGWHADAAABTTDKRNGAYTKYTTNNNNNTYRGVVTNTAARDG

A.t. AA-----GACTAAGTTTATA-CGT-----ACATTT-TATTTTAAGT
L.a. TATCAATATATTATA-GACAATATTTATAACGTTAAAAATACAATATTTATATTTTAT
B.n. TAACAGTGCAGTTTGGGTGGCTCTAAACAATGTCAAAGCTTCGACAAATAGTCTCTGGGA
* * * * *
Con. 4 WANNNNNNNNNNNNNGWSMDWVTWVAYANYGTNNNNNNNNNNAYAWWTNKWYTTDDRW

CE1

A.t. GGA-----AAACCGAAATT--TCCATCGAATATATGA--ATTT-AGTATAT---
L.a. ATATTTATTTCAAATTGAAAGCATTACTTCTATCGAAATGA--ATTTAGTATATTAAT
B.n. ACAC-----GCATCGACAGATACCCGGTCAAAATGATTCTGATTCAGGTAAGTCAGA
* * * * *
Con. 4 RBAYTNNNNNNRMAYYGAYADDYAYYMSDTCDAWMKWDAKMNNTTYNRGTAWRTNNNN

G-box2

A.t. --ATATTTCTGCAAT-----GTACTATTTTGCTATTTTGGCAA-CTTTCAGTGGACTAC
L.a. TAATATTTTAAATC-----GGACTACTTTCTATTTTGGCAC-CTTTCATCTGACTAC
B.n. GACTCGTGCCAAACGGTCCGTCTAATAACGATGTTGCTCTCTTTCGTTT--CTTT
* * * * *
Con. 4 NNMTMKTKYYBHAANNNNNNNGKMCTAHTWWVCKATKTTKGCMNCTTTCRKYKNNCTWY

G-box1

A.t. TACTTTATTACAATGTGT--ATGGATGC-ATGAG---TTTGAGTA-TACACATGCTCAAA
L.a. TAATTTATTTCAATGTGT--ATGCATGC-ATGAG---CATGAGTAATACACATGTCTATA
B.n. TTATTTGTTATAATAATTGATGGCTACGATGTTTCTCTTGTGTTGTTATGAATAAGAAT
* * * * *
Con. 4 TWMTTTRTTWYAATRWTNNATGSMTRCNATGWKNNNYWTGWKTRWTAYRMATRWKAWW

A-300 EM1 ABA

A.t. TGCATGCT-TTGCAAAACGTAACGGACC-ACAAAAGAGGATCCAATGCAAAATACATCTCAT
L.a. TAAATGCA-T-GTAAACGTAACGGACC-ACAAAAGTGGATCCATACAAATACATCTCAT
B.n. GCAATGGTGTCTAGTATTTGATTGTTTTACATGTATGTATCTCTT-ATTTACATGAAAT
* * * * *
Con. 4 KVMATGSWNTNSYARWAYKTRAYKGWYNNACAWRWRWGKATCYMTDNAWWTACATSWMAT

A.t. AGC-TTCCTCCATTATTTTCCGACACAAA-CAGAGCA---
L.a. CGC-ACCCTC-----TCCGACACAAAACCTGAACA---
B.n. TTTTAAACGCC-----TAAAAAATAACGGAATTCCG
* * * * *
Con. 4 HKYNWHMCKCNNNNNNNNNTMMRAMAMAAANCDGARYWNNN

Fig. 4C

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Figure 5- Alignment of A.t. and L.a. FAEI promoters
CLUSTAL W (1.74) multiple sequence alignment

```
A.t. -----ACTCATAA
L.a. CGCCGGGGAGTTTCAGCTTAACCGGTAAATGGCCTGTACATATATTTACCACTGAGTA
      ****
Con.5 ACTSAKWA

A.t. AACTAGTAGAT--TGGTTGGTTGGTTTCCA--TGTACCAGAAGGCTTACCCTATTAGTT
L.a. AAGACATCAGTTAATGATTTGTTGTTACTCAATTGGGCTAAGTGTATTATTATATGTGTT
      * * * * *
Con.5 AARMYAKYAGWTNNTGRTTKGTTGKTWYYCANNTGKRCYARRWGKMTTAYYMTATKWGTT

A.t. GAAAGTTGAAACTTTGTTCCCTACTCAATTCCTAGTTGTGTAAATGT---ATGTATATGT
L.a. GTATATAATAAAGGTAGAACGTAA--ATTTACTAAGAATGTGTTTTTCCAATGTGATTGC
      * * * * *
Con.5 GWAWRTWRWAAMKKTRKWMCMSTAMNNAWTTMCTARKWRTGTRWWTKTNNNATGTRWWTGY

A.t. AAT---GCGTATAAAACGTAGTACTTAAATGACTAGGAGTGGTTCTTGAGACCGATGAGA
L.a. TCTTTGGCCTCTTAGGTTTGAATCCTACTCGAGAAG-ACTAATTTTAATTACTGGCAA
      * * * * *
Con.5 WMTNNNGCSTMTWARRYKTRRWWCYTAMWYGASWAGNASTRRTTYTWRWKWMCKRKSARA

A.t. GATGGGAGCAGAACTAAAGATGATGACATAATTA-----AGAACGAATTTGAAAGG-CT
L.a. AATAGAAATCAATTTATAAGTGTTTAAACAAATCGATGGTATAACTGATTAGTGATCACT
      * * * * *
Con.5 RATRGRARYMRAWYTAWARRTGWTKAMAYAATWMTNNNNNNNAKAACKRATTGWRAKSNCT

A.t. CTTAGGTTTGAATCCTATTCGAGAATGTTTTTGTCAAAGATAGTGGCGATTTTGAACCAA
L.a. CTTAGGTTTGTATCCAACCTCGAGTATTGAGTATTGAACGCTT-----TTTTAAATAA
      * * * * *
Con.5 CTTAGGTTTKRATCCWAYTCGAGWATKKWKTWKTSAAMGMTWNNNNNNNTTTKAAMYAA

A.t. AGAAACATTTAAAAATCAGTATCCGGTTAC----GTTCATGCAATAGAAAGTGGTCT
L.a. AATCTTGATTTTAAATTGGTTTTTTGAGTAAAAAAGTTCTTAATATTTTCTCTTTGTTT
      * * * * *
Con.5 ARWMWWSATTTWAAAWTSRKTWYTYGRKTAMNNNGTTCWTRMWAWTWKMMWTKGTTT

A.t. A---GGATCTGATTGTAATTTTAGA--CTTAAAGAGTCTC--TTAAGATTCAATCCTGGC
L.a. TAATGGGTTTGTGTTTGCATTTTATAAGCTTAATTTTCTAATTTAATATTTATCTATCA
      * * * * *
Con.5 WNNNGGRTYTGWTTKKMATTTTAKANNCTTAAWKWKCTCMNNTTAAKATTYWATCYWKSMM

A.t. T-GTGTACAAAACCTACAAATAATATA----TTTTAGACTATTTGGCCTTAACTAAACTTC
L.a. TCGTCCGTAAAGTTTTATTTGGCACAACTTGTTTTACTTTTCTACCTTA--TAATTTGG
      * * * * *
Con.5 TNGTSYRYAAARYTWYAWWTRRYAYANNNTKTTWKACTWTTYKRCCTTANNTAAWYTKS

A.t. CA-CTCATTATTTACTGAGGTTAGAGAATAGACTTGCGAATAAACACATTCCCGAGAAAT
L.a. GAACCTGGTTGAGT-CAAAGCGTACCGGACAAATATGTTT-TATATTCTTATTTAAGAATT
      * * * * *
Con.5 SANCTSRTRWKTNCWRAGSKTASMGGRAYARAYWTGYKWNTAWAYWCWWTWYYRAGAAWT

A.t. -432 ACTCATGATCCCATAAATTAGTCAGAGGGSTATG-----CAATCAGATCTAAGAACA
L.a. AACACTCATCTCATAATTAGTCAGAGGCTAGGGAGATTGAGCCAATCAATGCTAACAACA
      * * * * *
Con.5 AMYMMTSATCYCATAATTAGTCAGAGGSTAKGNNNNNNNNNCCAATCARWKCTAASAACA
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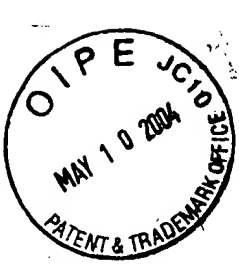
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A.t.	-381	CACATTCCCTCAA--ATTTTA--ATGCACATGTAATCAT-----AGTTT-----AGCA
L.a.		AA-ATTCTCTTAATGATCTAACGATGCT-ATTTAATATTCGGATCAGTATTCTTAAATAA * * * * *
Con.5		MANATTCTCYTYAANNATYTWANNATGCWNAKTAAATMTWNNNNNNNAGTWTNNNNNNNAKMA
A.t.	-337	CAATTCAAAAATAATGTAGTA-TTAAAGACAGAAATTTGTA--GACTTTTTT--TTGGCG
L.a.		GAATATAAAACTAATTCAATAGTTACAGATAAAAACTTATATAGACTTTTTTATTGGAA * * * * *
Con.5		SAATWYAAAAMTAATKYARTANTTAMAGAYARAAAYTTRTANNGACTTTTTTNTTGGMR
A.t.	-282	T-TAAAGGAA-----GACTAAGTTTATA-CGT-----ACATTT-TAT
L.a.		TATAAAAGTATCAATATATTATAGACAATATTTATAACGTTAAAAATACAATATTTATAT * * * * *
Con.5		TNTAAARGWANNNNNNNNNNNNGACWAWRTTATANCCTNNNNNNNNNNAYATTTNTAT
A.t.	-247	TTTAAGTGG-----AAACCGAAATT--TTCCATCGAAATATATGAATTT-AGTATA
L.a.		TTTTTATATATTTTATTTCAAATTGAAAAGCATTACTTCTATCGAAATGAATTTTAGTATA * * * * *
Con.5		TTTWWRTRKANNNNNNNNNAAAYYGAAWKNNTTMCWTCKAWMKAWATGAATTTNAGTATA
A.t.	-198	T-----ATATTTCTGCAAT-GTACTATTTTGCTATTTTGGCACTTTCAGTGGACTACT
L.a.		TTAATTAATATTTTATTTAATCGGACTACTTTCCTATTTTGGCACCTTTCATCTGACTACT * * * * *
Con.5		TNNNNNNATATTTTYTKYAATNGKACTAYTTTSCATTTTGGCAMECTTCAKYKGACTACT
A.t.	-145	ACTTTATTACAATGTGTATGGATGCATGAGTTTGAGTA-TACACATGCTCAAATGCATGC
L.a.		AATTTATTTCAATGTGTATGCATGCATGAGCATGAGTAATACACATGCTATATAAATGC * * * * *
Con.5		AMTTTATTWCAATGTGTATGSATGCATGAGYWTGAGTANTACACATGCTAWATRMATGC
A.t.	-86	TTTGCAAAACGTAACGGACCACAAAAGAGGATCCATGCAAATACATCTCATAGCTTCCCTC
L.a.		AT-GTAAAACGTAACGGACCACAAAAGTGGATCCATACAAATACATCTCATCGCACCCTC * * * * *
Con.5		WTNGYAAAACGTAACGGACCACAAAAGWGGATCCATRCAAATACATCTCATMGWCWYCCTC
A.t.	-26	CATTATTTTCCGACACAAA-CAGAGCA
L.a.		-----TCCGACACAAAACCTGAACA * * * * *
Con.5		NNNNNNNTCCGACACAAANCWGARCA

FIG. 5B



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Figure 6

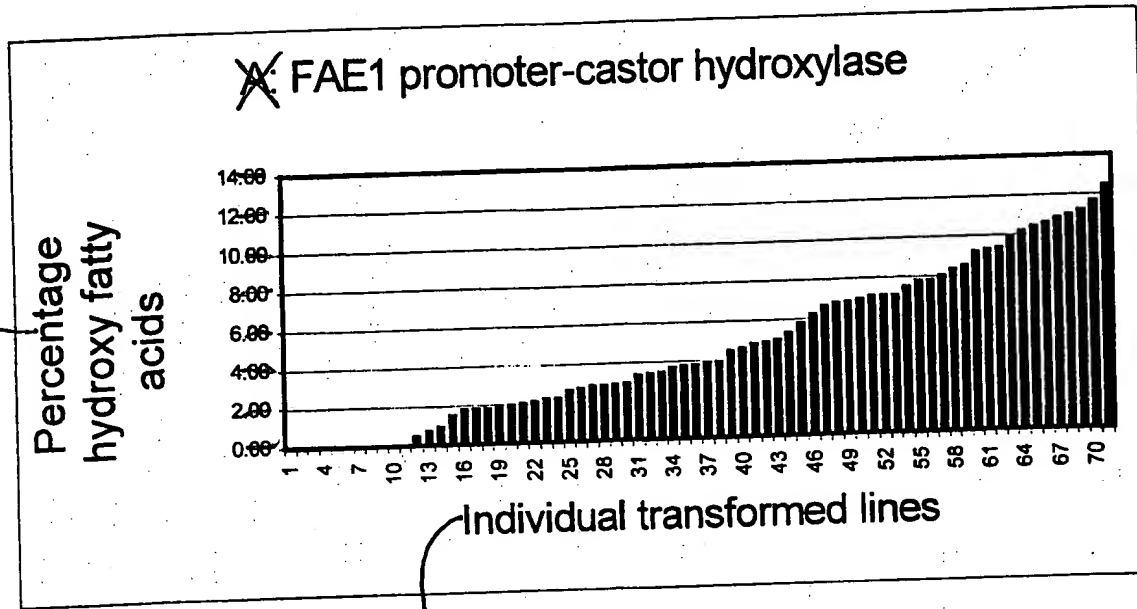


FIG. 6A

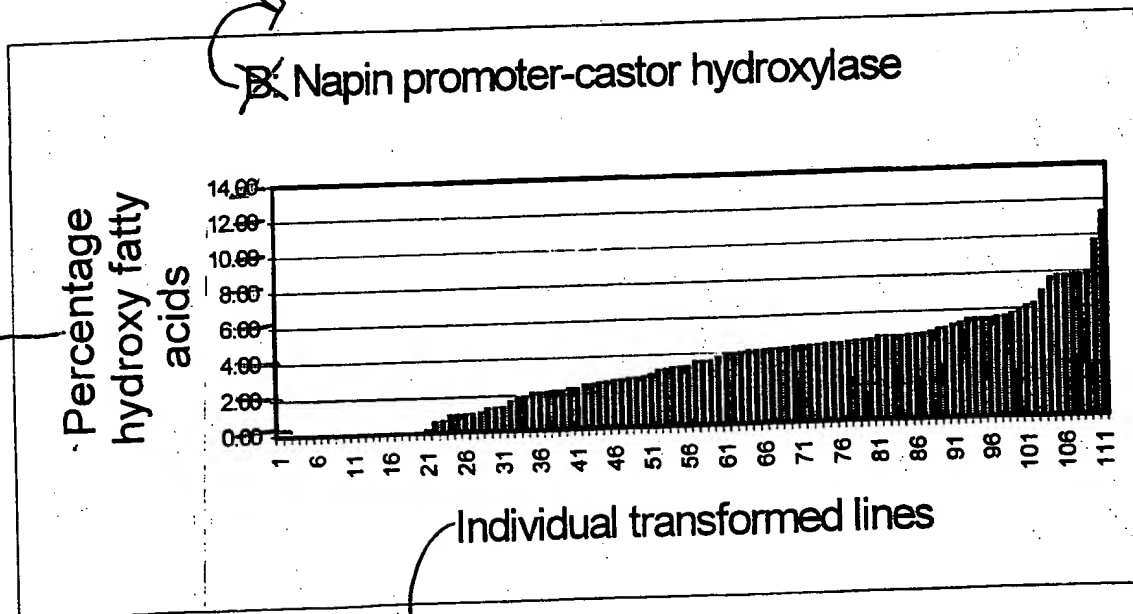


FIG. 6B

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~~Figure 7:~~ Alignment of *B.n.* and *L.a.* *FAE1* promoters

CLUSTAL W (1.81) multiple sequence alignment

```
BnFAE1      GGTGGGCAAATCTGACTTCACCAAAGAAACAACCTCGAGTCGTTATCCATCTCCTCATAA 60
LaFAE1      -----

BnFAE1      CCATCGCTCCACTCTTTGCCTTCACCGTTTTTCGGTTCGGTTCTCTACATCGCAACCCGGC 120
LaFAE1      -----

BnFAE1      CCAAACCGGTTTACCTCGTTGAGTACTCATGCTACCTTCCACCAACGCATTGTAGATCAA 180
LaFAE1      -----CGCCGGGGAGT-TCAGCTTAACCGGTAAAATTGGCCTGTACATATA 46
              *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *

BnFAE1      GTATCTCCAAGGTCATGGATATCTTTTATCAAGTAAGAAAAGCTGATCCTTCTCGGAACG 240
LaFAE1      TTTACCACTGAGT-AAAGACATCAGTTAATGATT-----GTTGTTACTCAATTGGGCT 99
              *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *

BnFAE1      GCACGTGCGATGACTCGTCGTGGCTTGACTTCTTGAGGAAGATTCAAGAACGTTCCAGGTC 300
LaFAE1      AAGTGTATTATTATATGTGTG-----TATATAATAAAGGT---AGAACGT--AAATT 147
              *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *

BnFAE1      TAGGCGATGAAACTCACGGGCCGAGGGGCTGCTTCAGGTCCCTCCCGGAAGACTTTTG 360
LaFAE1      TA--CTAAGAATGTGTTTTTCCAATGTGATTGCTCTTTGGCCTCTTAGGTTTGAATCCTA 205
              *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *

BnFAE1      CGGCGGCGCGTGAAGAGACGGAGCAAGTTATCATTGGTGCGCTAGAAAATCTATTCAAGA 420
LaFAE1      CT-----CGAGAAGACTAATTTTAAT-TTACTGGCAAAAATAGAAATCAATTTATAA 256
              *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *

BnFAE1      ACACCAACGTTAACCCCTAAAGATATAGGTATACTTGTGGTGAAGTCAAGCATGTTTAAATC 480
LaFAE1      GTGTTTAAACAAATC--GATGGTATAACTG-ATTAGTGATCACTCTTAGGTT--TTGATC 311
              *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *

BnFAE1      CAACTCCATCGCTCTCCGCGATGGTCGTTAACTTTCAAGCTCCGAAGCAACGTAAGAA 540
LaFAE1      CAACTCGAGTATTG-----AGTATTGAACGCTTT-----TTTTAAATAAAATCTTGA 358
              *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *

BnFAE1      GCTTTAACCTTGGTGGCATGGGTTGTAGTGCCGCGCTTATAGCCATTGATCTAGCAAAGG 600
LaFAE1      TTTTAAA-TTGGTTTTTTGGAGTAAAAAGTTCTTAATATTTTCTCTT-TGTTTTAATGG 416
              *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *

BnFAE1      ACTTGTTCATGTCC-ATAAAAATACGSTATGCTCTTGTGGTGAGCACAGAGAATCACT 659
LaFAE1      GTTTGTTTTGCATTTTATAAGCTTAATTTTCTAATTTAAT-ATTTTATCATCATCGTC 475
              *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *

BnFAE1      TATAACATTTACGCTGGTGATAATAGGTCCATGATGGTTTTCAAATTGCTTGTTCGGTGT 719
LaFAE1      CGTAAAGTTT-----TATTTGGCACAACTTGTTTTA---CTTTTCTACCTTATA 522
              *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *

BnFAE1      GGTGGGGCCGCTATTTTGTCTCTCCAACAAGCCTGGAGATCGTAGACGGTCCAAGTACGAG 779
LaFAE1      ATTTGGGA-ACTGGTTGAGTCA-----AAGCGTACCGGACAAATATGTTTATATTC--- 573
              *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *

BnFAE1      CTAGTTCACACGGTTCGAACGCATACCGGAGCTGACGACAAGTCTTTTCGTTGCGTGCAA 839
LaFAE1      -TTATTTA-AGAATTAACACTCATCTCATAATTAGTCAGAGGC-----TAGGGAGATT 624
              *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *

BnFAE1      CAAGGAGACGATGAGAACGGCAAAATCGGAGTGAGTTTGTCCAAGGACATAACCGATGTT 899
LaFAE1      CAGCCAATCAATGCTAACCAAAATTTCTTTAA--TGATCTAACGATGCTATTTAATAT 682
              *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *
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~~Figure 7 Continued~~: Alignment of *B.n.* and *L.a.* *FAE1* promoters

BnFAE1	GCTGGT CGAACGGTTAAGAAAAACATAGCAACGTTGGGTCCGTTGATTCTTCCGTTA-AG	958
LaFAE1	TCGGATCAGTATTCTTAAATAAGAAATATAAA-----ACTAATTCAATAGTTACAG	732
	* * * * *	
BnFAE1	CGAGAAACTTCTTTTTTCGTTACCTTCATGGGCAAGAAACTTTTCAAAGATAAAATCAA	1018
LaFAE1	ATAAAACTTATATAGACTTTTTTATTG-GAATATAAAAGTATCAATATATTATAGACA	791
	* * * * *	
BnFAE1	ACATTACTACGTCCCGGATTTCAACTTGCTATTGACCATTTTGTATACATGCCGGAGG	1078
LaFAE1	ATATTTATA-----ACGTTAAAAATACAATTTTATATTTTATATATTTATTTCAAA	845
	* * * * *	
BnFAE1	CAGAGCCGTGATTGATGTGCTAGAGAAGAACCTAGCCCTAGCACCGATCGATGTAGAGGC	1138
LaFAE1	TTGAAAAGCATTACTTCTATCGAAATGAATTTTAGT-----ATATTAATTAATATTTTTT	901
	* * * * *	
BnFAE1	ATCAAGATCAACGTTACATAGATTTGGAAACACTTCATCTAGCTCAATATGGTATGAGTT	1198
LaFAE1	AATCGGACTACTTTCCTAT-----TTTGGCACCTTCATCTGACT-----ACT	944
	* * * * *	
BnFAE1	GGCATACATAGAAGCAAAAGGAAGGATGAAGAAAGGTAATAAAGTTTGGCAGATTGCTTT	1258
LaFAE1	AATTTATTTCAATGTGTATGCATGCATGAGCATGAGTAATA-----CACATGCTAT	996
	* * * * *	
BnFAE1	AGGGTCAGGCTTTAAGTGTAAACAGTGCAGTTTGGGTGGCTCTAAACAATGTCAAAGCTTC	1318
LaFAE1	ATAAATGCATGTAAACGTAACGG-ACCACAAAAGTGGATCCATACAAATACATCTCATC	1055
	* * * * *	
BnFAE1	GACAAATAGTCCTTGGGAACACTGCATCGACAGATACCCGGTCAAATGATTCTGATTC	1378
LaFAE1	G-CACCCCTCTCCGACACAAAACGAACA-----	1082
	* * * * *	
BnFAE1	AGGTAAGTCAGAGACTCGTGTCCAAAACGGTCGGTCCTAATAAACGATGTTTGCTCTCTT	1438
LaFAE1	-----	
BnFAE1	TCGTTTCTTTTTATTGTTATAATAATTTGATGGCTACGATGTTTCTCTGTTTGTATG	1498
LaFAE1	-----	
BnFAE1	AATAAAGAATGCAATGGTGTCTAGTATTTGATGTTTTACATGTATGTATCTCTTATT	1558
LaFAE1	-----	
BnFAE1	ACATGAAATTTTAAACGCCTAAAAAACAACCGAATTCCG	1600
LaFAE1	-----	

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Figure 8: Alignment of *B.n.* and *A.t.* *FAE1* promoters

CLUSTAL W (1.81) multiple sequence alignment

AtFAE1
BnFAE1

GGTTGGGCAAATCTGACTTCACCAAAGAAACAACTCGAGTCGTTATCCATCTCCTCATAA 60

AtFAE1
BnFAE1

CCATCGCTCCACTCTTTGCCTTCACCGTTTTTCGGTTCGGTTCCTACATCGCAACCCGGC 120

AtFAE1
BnFAE1

CCAAACCGGTTTACCTCGTTGAGTACTCATGCTACCTTCCACCAACGCATTGTAGATCAA 180

AtFAE1
BnFAE1

-----ACTCATAAAA 10
GTATCTCCAAGGTCATGGATATCTTTTATCAAGTAAGAAAAGCTGATCCTTCTCGGAACG 240
*** **

AtFAE1
BnFAE1

ACTAGTAGATTGGTTGGT--TGGTTTCCATGTACCAGAAGGCTT-----ACCCTATTAGT 63
GCACGTGCGATGACTCGTCGTGGCTTGACTTCTTGAGGAAGATTCAGAACGTTCCAGGTC 300
* ** * * * * * * * * * * * * *

AtFAE1
BnFAE1

TGAAAGTTGAAACTT-TGTTCCCTACT--CAATTCCTAGTTGTGTAAATGTATGTATATG 120
TAGGCGATGAAACTCACGGGCCCCGAGGGGCTGCTTCAGGTCCTCCCGGAAGACTTTTG 360
* * * * * * * * * * * * * * *

AtFAE1
BnFAE1

TAATG-CGTATAAAACGTAGTACTTAAATGACTAGGAGTGGTCTTGAGACCGATGAGAG 179
CGGCGGCGCGTGAAGAGACGGAGC-AAGTTATCATTGGTGCCTAGAAAATCTATTCAAG 419
* * * * * * * * * * * * * * *

AtFAE1
BnFAE1

A----TGGGAGCAGAACTAAAGATGATGACATAATTAAGAACGAATTTGAAAGGCTCTTA 235
AACACCAACGTTAACCTTAAAGATATAGGTATACTTGTGG-TGAACCTCAAGCATGTTTAA 478
* * * * * * * * * * * * * * *

AtFAE1
BnFAE1

GGTTTGAATCCTATTTCGAGAATGTTTTGTCAAAGATAGTGGCGA-TTTGAACCAAAGA 294
---TCCAACCTCATCGCTCTCCGCGATGGTTCGTTAACACTTTCAGCTCCGAAGCAACGT 535
* * * * * * * * * * * * * * *

AtFAE1
BnFAE1

AAACATTTAAAAATCAGTATCC--GGTTAC-GTTCATGCAA-ATAGAAAGTGGTCTAGG 350
AAGAAGCTTTAACCTTGGTGGCATGGGTTGTAGTGCCGCGGTTATAGCCATTGATCTAGC 595
* * * * * * * * * * * * * * *

AtFAE1
BnFAE1

ATCTGATTGTAATTTTAGACTTAAAGAGTCTCTTAAGATTCAATCCTGGCTGTGTACAAA 410
AAAGGACTT--GTTGCATGTCCATAAAAATACGTATGCTCTTGTGGTGAGCACAGAGAAC 653
* ** * * * * * * * * * * * * *

AtFAE1
BnFAE1

ACTACAAATAATATAT---TTTAGACTATTTGGCCTTAACTAAACTTCCACTCATTATTT 467
ATCACTTATAACATTTACGCTGGTGATAATAGGTCCATGATGGTTTCAATTGCTTGCTC 713
* ** * * * * * * * * * * * * *

AtFAE1
BnFAE1

ACTGAGGTTAGAGA-ATAGACTTGCGAATAAACACATTCCCGAGAAATACTCATGATCCC 526
CGTGTGTTGGTGGGGCCGCTATTTTGTCTCTCCAACAAG--CCTGGAGATCGTAGACGGTCCA 771
* * * * * * * * * * * * * * *

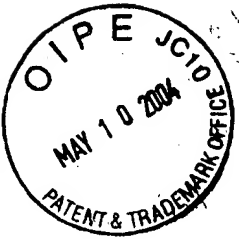
CE3

AtFAE1
BnFAE1

ATAATTAGTCAGAGGGTATG--CCAATCAGATCTAAGAACACACATTCCTCAATTTTA 584
AGTACGAGCTAGTTCACACGGTTCGAACGCATACCGGAGCTGACGACAAGTCTTTTCGTT 831
* * * * * * * * * * * * * * *

AtFAE1
BnFAE1

ATGCACATGTAATCATAGTTTAGCACAATTCAAAAATAATGTAGTATTAAAGACAGAAAT 644
GCGTGCAACAGGAGACGATGAGAACGGCAAAATCGGAGTGAGTTTGTCCAAGGACATAA 891



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Figure 8 Continued: Alignment of *B.n.* and *A.t.* *FAE1* promoters

AtFAE1	TTGTAGACTTTTTTTTGGCGTTAAAGGAAGACTAAG-----TTTATACGTACATTTTAT	698
BnFAE1	CCGATGTTGCTGGTCAACGGTTAAGAAAAACATAGCAACGTTGGGTCCGTTGATTCTTC	951
	* * * * *	
AtFAE1	T-TTAAGTGGAAAACCGAAATTTTCCAT-----CGAAATATATGAATTAGTATATATA	751
BnFAE1	CGTTAAGCGAGAAACTTCTTTTTTTCGTTACCTTCATGGGCAAGAACTTTTCAAAGATA	1011

	G box 2	
AtFAE1	TTTCTGCAATGTACTATTTTGCTATTTTGGCAACTTTCAGTGGACTACTACTTTAT-TAC	810
BnFAE1	AAATCAAACATTACTACGTCCCGGATTTC-AACTTGCTATTGACCATTTTGTATACAT	1070
	* * * * *	
	G-box 1	
AtFAE1	AATGTGTATGGATGCGATGAGTT-TGAGTATACACATGTCTAAATGCATGCTTTGCAAAAC	869
BnFAE1	GCCGGAGGCAGAGCCGTGATTGATGTGCTAGAGAAGAACCTAGCCCTAGCACCAGATCGAT	1130
	* * * * *	
AtFAE1	GTAACGG-ACCACAAAAGAGGATCCAT-----GCAAATACATCTCATAGCTTCTCTCCAT	922
BnFAE1	GTAGAGGCATCAAGATCAACGTTACATAGATTGGAAACACTTCATCTAGCTCAATATGG	1190
	*** * * * *	
AtFAE1	TATTTTCCGACACAAACAGA-GCA-----	945
BnFAE1	TATGAGTTGGCATACATAGAAGCAAAGGAAGGATGAAGAAAGGTAATAAGTTTGGCAG	1250
	*** * * * *	
AtFAE1	-----	
BnFAE1	ATTGCTTTAGGGTCAGGCTTTAAGTGTAACAGTGCAGTTTGGGTGGCTCTAAACAATGTC	1310

AtFAE1	-----	
BnFAE1	AAAGCTTCGACAAATAGTCCTTGGGAACACTGCATCGACAGATACCCGGTCAAATTGAT	1370

AtFAE1	-----	
BnFAE1	TCTGATTCAGGTAAGTCAGAGACTCGTGTCCAAACGGTCGGTCCTAATAAACCAGTGT	1430

AtFAE1	-----	
BnFAE1	GCTCTCTTCGTTTCTTTTATTGTTATAATAATTTGATGGCTACGATGTTTCTCTTGT	1490

AtFAE1	-----	
BnFAE1	TTGTTATGAATAAAGAATGCAATGGTGTCTAGTATTGATTGTTTACATGTATGTATC	1550

AtFAE1	-----	
BnFAE1	TCTTATTTACATGAAATTTTAAACGCCTAAAAAACAACGGAATTCCG	1600

Fig. 8B

